

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2003, 20:06:37 ; Search time 21 Seconds

(without alignments)  
1159.362 Million cell updates/sec

Title: US-09-815-923-4

Perfect score: 3141

Sequence: 1 MPPSDAPPAPAPPPDLPAT.....TIOREPTVSTPPADSLCNL 587

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

1 number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2333.5	74.3	622	1 S6A4_DROME	P51905 drosophila
2	1726	55.0	630	1 S6A4_HUMAN	P31645 homo sapien
3	1723	54.9	630	1 S6A4_CAVPO	O35899 cavia porce
4	1717	54.7	630	1 S6A4_MACMO	O9mwx0 macaca mula
5	1716	54.6	630	1 S6A4_MOUSE	O60852 mus musculu
6	1712	54.5	630	1 S6A4_RAT	P31652 rattus norv
7	1706	54.3	630	1 S6A4_BOVIN	O9x449 bos taurus
8	1629.5	51.9	617	1 S6A2_MOUSE	O55192 mus musculu
9	1608.5	51.2	615	1 S6A2_BOVIN	P51143 bos taurus
10	1605.5	51.1	617	1 S6A2_HUMAN	P23975 homo sapien
11	1558	49.6	693	1 S6A3_BOVIN	P27922 bos taurus
12	1542	49.1	620	1 S6A3_HUMAN	O01959 homo sapien
13	1539	49.0	619	1 S6A3_RAT	P23977 rattus norv
14	1538	49.0	619	1 S6A3_MOUSE	O61327 mus musculu
15	1412	45.0	615	1 NTDO_CAEEL	O03614 caenorhabdi
16	1368.5	43.6	797	1 S6A5_HUMAN	O9y945 homo sapien
17	1363.5	43.4	799	1 S6A5_RAT	P58295 rattus norv
18	1358.5	43.3	599	1 S6A1_HUMAN	P30531 homo sapien
19	1347.5	42.9	598	1 S6A1_RAT	P23978 rattus norv
20	1329	42.3	598	1 S6A1_MOUSE	P48057 mus musculu
21	1309	41.7	598	1 S6A1_MOUSE	P31645 mus musculu
22	1298	41.3	635	1 S6A8_BOVIN	O18875 bos taurus
23	1286.5	41.0	635	1 S6A8_HUMAN	P48029 homo sapien
24	1282	40.8	620	1 S6A8_RAT	P28570 rattus norv
25	1279	40.7	635	1 S6A6_BOVIN	O9m234 bos taurus
26	1279	40.7	635	1 S6A8_RABIT	P31661 oryctolagus
27	1271	40.5	627	1 S6A6_RAT	P31647 rattus norv
28	1268	40.4	627	1 S6A6_MOUSE	P31650 mus musculu
29	1267	40.3	620	1 S6A6_CANFA	O00589 canis famli
30	1256.5	40.0	614	1 S6A6_MOUSE	P27799 canis famli
31	1254	39.9	602	1 S6A6_RAT	P31646 rattus norv
32	1253.5	39.9	632	1 S6A6_HUMAN	P48066 homo sapien
33	1252	39.9	602	1 S6A6_MOUSE	P31649 mus musculu

34	1251.5	39.8	614	1 S6A6_RAT	P48056 rattus norv
35	1251	39.8	620	1 S6A6_HUMAN	P31641 homo sapien
36	1247.5	39.7	614	1 S6A6_HUMAN	P48065 homo sapien
37	1244.5	39.6	614	1 S6A6_RABIT	P48055 oryctolagus
38	1243	39.6	614	1 S6A6_MOUSE	P31651 mus musculu
39	1243	39.6	621	1 S6A6_RAT	P31643 rattus norv
40	1241	39.5	621	1 S6A6_MOUSE	P31642 mus cookli
41	1238.5	39.4	637	1 S6A7_RAT	P28573 rattus norv
42	1232.5	39.2	636	1 S6A7_HUMAN	O99884 homo sapien
43	1229	39.1	638	1 S6A9_BOVIN	O28039 bos taurus
44	1221	38.9	621	1 S6A6_MOUSE	O35316 mus musculu
45	1212	38.6	633	1 S6A9_RAT	P28572 rattus norv

## ALIGNMENTS

RESULT 1	ID	Sequence	Standard	PRT	622 AA
AC	S6A4_DROME	09W1177:			
DT	01-OCT-1996 (rel. 34, Last sequence update)				
DT	01-OCT-1996 (rel. 34, Last sequence update)				
DT	16-OCT-2001 (rel. 40, Last annotation update)				
DE	Sodium-dependent serotonin transporter (5HT transporter) (5HTT)				
DE	(Cocaine-sensitive serotonin transporter).				
GN	SERT OR CGA545.				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;				
OC	Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;				
OX	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
OX	NCBI_Taxid=7227;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Canlon-S; TISSUE=Head;				
RC	MEDLINE=94255490; PubMed=8197200;				
RA	Demchynshyn L.L., Pristupa Z.B., Sugamori K.S., Barker E.L.,				
RA	Blakely R.D., Wolfgang W.J., Forte M.A., Niznik H.B.;				
RT	*Cloning, expression, and localization of a chloride-facilitated,				
RT	cocaine-sensitive serotonin transporter from Drosophila				
RT	melanogaster.;				
RT	Proc. Natl. Acad. Sci. U.S.A. 91:5158-5162(1994).				
RT	[2]				
RC	SEQUENCE FROM N.A.				
RC	STRAIN=Berkely;				
RC	MEDLINE=20196006; PubMed=10731132;				
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,				
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,				
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,				
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,				
RA	Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,				
RA	Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,				
RA	Abdel J.F., Agayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,				
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,				
RA	Beeson K.Y., Benos P.V., Bernack B.P., Bhandari D., Bolshakov S.,				
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,				
RA	Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,				
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,				
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,				
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,				
RA	Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,				
RA	Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,				
RA	Glocke A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,				
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,				
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,				
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,				
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,				
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,				
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,				
RA	Merkulov G., Mikhlin N.V., Mobarry C., Morris J., Moshrefi A.,				
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,				
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,				
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,				



CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR  
 CC STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.  
 CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER  
 CC FAMILY (SNF).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: X70697; CAA50029.1; -  
 CC EMBL: L05568; AAA35492.1; -  
 CC EMBL: U79746; AAB93475.1; -  
 CC PIR: S37688; S37688.  
 CC PIR: A47398; A47398.  
 CC GeneW: HGNC:11050; SLC6A4.  
 CC MIM: 182138; -  
 CC InterPro: IPR002437; 5HT\_transporter.  
 CC InterPro: IPR000175; Na/ntran\_symport.  
 CC Pfam: PF00209; SNF; 1.  
 CC PRINTS: PR00176; NANEUSMPORT.  
 CC ProDom: PD000448; Na/ntran\_symport; 1.  
 CC PROSITE: PS00610; NA\_NEUROTRAN\_SYM\_1; 1.  
 CC PROSITE: PS00754; NA\_NEUROTRAN\_SYM\_2; 1.  
 CC PROSITE: PS0267; NA\_NEUROTRAN\_SYM\_3; 1.  
 CC Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;  
 CC Symport.  
 CC KM  
 CC DOMAIN 1 87 108 CYTOPLASMIC (POTENTIAL).  
 CC FT TRANSMEM 8 87 108 1 (POTENTIAL).  
 CC FT TRANSMEM 116 135 2 (POTENTIAL).  
 CC FT TRANSMEM 160 180 3 (POTENTIAL).  
 CC FT DOMAIN 181 252 EXTRACELLULAR (POTENTIAL).  
 CC FT TRANSMEM 253 271 4 (POTENTIAL).  
 CC FT TRANSMEM 280 297 5 (POTENTIAL).  
 CC FT TRANSMEM 333 350 6 (POTENTIAL).  
 CC FT TRANSMEM 362 383 7 (POTENTIAL).  
 CC FT TRANSMEM 417 436 8 (POTENTIAL).  
 CC FT TRANSMEM 464 482 9 (POTENTIAL).  
 CC FT TRANSMEM 498 518 10 (POTENTIAL).  
 CC FT TRANSMEM 539 558 11 (POTENTIAL).  
 CC FT TRANSMEM 577 595 12 (POTENTIAL).  
 CC FT DOMAIN 596 630 CYTOPLASMIC (POTENTIAL).  
 CC FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CARBOHYD 217 217 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC SEQUENCE 630 AA; 70324 MW; 0EB535B0A579BDA2 CRC64;  
 CC -----  
 CC Query Match 55.0%; Score 1726; DB 1; Length 630;  
 CC Best Local Similarity 54.5%; Pred. No. 6, 2e-106;  
 CC Matches 320; Conservative 97; Mismatches 154; Indels 16; Gaps 6;  
 CC  
 CC 6 APPAPTAAPP---DLPATTAQKRSVVVSLPFARORETMAKAEFLAVGVADLGNW 62  
 CC 1  
 CC 49 AVPSYGADDDRRHSIPATT-----TTVAELHGGRETRGKVDLLSLVIGAVDLGNW 103  
 CC 1  
 CC 63 RPPYCYONGGAGFLPYCVMLFEGGLPFELELAGOYHRCGLTLMKRICPALKGVGY 122  
 CC 1  
 CC 104 RPPYCYONGGAGFLPYTIMAFEGIDPLFYEMELALGOYHRCGICISIMKICPIKFGIGY 163  
 CC 1  
 CC 123 AICMIDIMGMVYNTIIMAVYLLASLASINSVLPWISCDENMTPLCTPPTSPT--- 179  
 CC 1  
 CC 164 AICIIAFIASYNTIIMAVLYLL---SSFTDLPWISCKKSNMTGCTNTFYSSDNTIW 220  
 CC 1  
 CC 180 NPNSTPAKKEFFERNVLEOHKSGNGLDMGPIKPSLALCVFVLYVFSLMKGVASAKV 239  
 CC 1  
 CC 221 TLHSTSPAEFEYTRIVLDIHRKSGIDLDLGISIQWALCLMLFIYIYSIMKGVATSGKV 280  
 CC 1  
 CC 240 VWTATLAPYVLLILLARGVTLPGATEGIRYYLTFEMHKLONSKYVDAASOIFPSLGP 299  
 CC 1

DB 281 VWTATPFIILSYLLVVGATLPGAMRGVLFYLPKPNMOKLLETGVWIDAQAIFPSLGP 340  
 QY 300 FCTLLALSYNKFNKNCRDALITSINCITSFLAGPIYFSLVGLGMANVOKNSTEVL 359  
 DB 341 FGVLLAFASYNKFNKNCYODALVTSVNCMTSFVSGFVIFVLGYMAEMRNDSEVAKD 400  
 QY 360 -GGVLFVYPPAATMTMGVFWALITPFLMLTLTLDSPFGLLEVNTALCDEYRIVGR 418  
 DB 401 AGPSLFTFYEAALINMASTFAITPFLMLTLTLDSTFAGLEVITRAVDEPFVNAK 460  
 QY 419 HREVEVAVLLFTYICALPTTYGGVYLVDLLNVYGPGLAILFVFAEAGVGVYDVR 478  
 DB 461 RREVEVAVLITCFGSLVTLTFPGAYVVKLLEEYATGPVLTVALIAVAVSWFEGITQ 520  
 QY 479 PSEDVRYMLGHRPGFWFRWCWISIPVLLVLFVPSVLAHEMLGCEYTPSNSTVGV 538  
 DB 521 FCRDVKEMIGFSGFWFMRICWVAISPFLPLFTICSLFSLSPQLRFLFYNYPSIILGYC 580  
 QY 539 MTGTVVSCIPLYIYKLLITPNCINR-IKTIOREPVTSIPADSTL 584  
 DB 581 ICTSSFICLPITYIARLLITPCTFRERIKISTTPETPIEIPCGDIRL 627  
 RESULT 3  
 S6A4\_CAVPO  
 ID S6A4\_CAVPO STANDARD: PRT: 630 AA.  
 AC 035899:  
 DT 15-JUL-1998 (rel. 36, Created)  
 DT 15-JUL-1998 (rel. 36, Last sequence update)  
 DT 16-OCT-2001 (rel. 40, Last annotation update)  
 DE Sodium-dependent serotonin transporter (5HT transporter) (5HTT).  
 GN SLC6A4.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Intestinal mucosa;  
 RX MEDLINE=96180949; PubMed=8601815;  
 RA Wade P.R., Chen J., Jaffe B., Kassem I.S., Blakely R.D., Gershon M.D.;  
 RT "Localization and function of a 5-HT transporter in crypt epithelia  
 RT of the gastrointestinal tract.";  
 RT J. Neurosci. 16:2352-2364(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Intestinal mucosa;  
 RA Chen J., Wade P.R., Rothman T.P., Gershon M.D.;  
 RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: TERMINATES THE ACTION OF SEROTONINE BY ITS HIGH  
 CC AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR  
 CC STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.  
 CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER  
 CC FAMILY (SNF).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: U84498; AAB82737.1; -  
 CC InterPro: IPR002437; 5HT\_transporter.  
 CC InterPro: IPR000175; Na/ntran\_symport.  
 CC Pfam: PF00209; SNF; 1.  
 CC PRINTS: PR00176; NANEUSMPORT.  
 CC ProDom: PD000448; Na/ntran\_symport; 1.  
 CC PROSITE: PS00610; NA\_NEUROTRAN\_SYM\_1; 1.

DR PROSITE: PS00754; NA\_NEUROTAN\_SYM\_2; 1.  
 DR PROSITE: PS0267; NA\_NEUROTAN\_SYM\_3; 1.  
 KW Neurotransmitter transport; Transmembrane; Glycoprotein;  
 Symport.  
 FT DOMAIN 1 87 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 88 108 1 (POTENTIAL).  
 FT TRANSMEM 116 135 2 (POTENTIAL).  
 FT TRANSMEM 160 180 3 (POTENTIAL).  
 FT DOMAIN 181 252 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 253 271 4 (POTENTIAL).  
 FT TRANSMEM 280 297 5 (POTENTIAL).  
 FT TRANSMEM 333 350 6 (POTENTIAL).  
 FT TRANSMEM 362 383 7 (POTENTIAL).  
 FT TRANSMEM 417 436 8 (POTENTIAL).  
 FT TRANSMEM 464 482 9 (POTENTIAL).  
 FT TRANSMEM 498 518 10 (POTENTIAL).  
 FT TRANSMEM 539 558 11 (POTENTIAL).  
 FT TRANSMEM 577 595 12 (POTENTIAL).  
 FT DOMAIN 596 630 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 217 217 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SEQUENCE 630 AA; 70113 MW; EE2A717DD926D2F CMC64;

Query Match Best Local Similarity 54.9%; Score 1723; DB 1; Length 630;  
 Matches 308; Conservative 99; Mismatches 138; Indels 8; Gaps 4;

OY 37 QRETKAKAEFLAVAVGAVDGLGVNVRPPYCYONGGAFILPYCVMLFGPLFLEL 96  
 DB 78 ERETKGKVDLSTIGAVDGLGNTRPPYCYONGGAFILPYCVMLFGPLFLEL 137  
 OY 97 ALGOYHRCCLTLMKRICPALGVGVAICMIDYGMVYNTLIGNAVYLLASLASINSV 156  
 DB 138 ALGOYHRCCLTLMKRICPALGVGVAICMIDYGMVYNTLIGNAVYLLASLASINSV 194  
 OY 157 LPMVSCDENVTPCTPYTSPT---NNSSIPAEFEFRNVLEDKHSGNDMDKPIPS 213  
 DB 195 LPMVSCDENVTPCTPYTSPT---NNSSIPAEFEFRNVLEDKHSGNDMDKPIPS 254  
 OY 214 LALCVGVFLVYFLMKVRSAGKVVWVMTALAPVLLILLARGVTLPGATEGRYVLT 273  
 DB 255 LTLCLMLFTIIVYSIMKGVKTSKVVWVMTAFPIIVSVLLVKGATLPGAMKGVLFVK 314  
 OY 274 PEMHKLONSKYVIDAASQIFPSLGFPGFTLLALLSYNNFNKNCYDALITSSINCLTSP 333  
 DB 315 PMOKLLETGVVIDAAQIFPSLGFPGFTLLALLSYNNFNKNCYDALITSSINCLTSP 374  
 OY 334 AGFVFFSLGYMAHYNKNSIEVGLG-GRGLVFIYPPALATMGVSVMATIFFLMLTL 392  
 DB 375 SGFVLFYLVGYMAERSEDEVAVDAGPSLFLTYAALANMPASTFEAIFFLMLTL 434  
 OY 393 GLDSTFGGLAVNTALCDEYPRVLGRHREVEVAVLLFLYICALPTTYGGVYVLDLNV 452  
 DB 435 GLDSTFGGLAVNTALCDEYPRVLGRHREVEVAVLLFLYICALPTTYGGVYVLDLNV 494  
 OY 453 YGPGALIFVVPAAAGVCMVYGVDRSEDEVATMLGHTPGMFWRTQMSYISPVFLLEV 512  
 DB 495 YATGPAVLTVFIEALVASMFEYGVQFCSYKEMLGSPGFMFRICWAVSPVFLFLIC 554  
 OY 513 FSVLAHEMLGGEYTPMSITVGVMGTIVSCPLIITIKLLITPNCINR-IKTQR 571  
 DB 555 SFLMSPPQLRLFOYSYPMHVSILGYCIGTSSVICPIYITRYLVLTPTGLKERIKSTIP 614  
 OY 572 PEVTSIPPADSTL 584  
 DB 615 ETPTEIPGCDICL 627

RESULT 4  
 ID S6A4\_MACMU STANDARD: PRT: 630 AA.  
 AC O9MYXO-16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Sodium-dependent serotonin transporter (5HT transporter) (5HTT).  
 GN SLC6A4.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Midbrain;  
 RX MEDLINE=21126513; PubMed=11223167;  
 RA Miller G.M., Yatin S.M., De la Garza R. II, Goulet M., Madras B.K.:  
 FT "Cloning of dopamine, norepinephrine and serotonin transporters from  
 RL monkey brain: relevance to cocaine sensitivity.";  
 CC Brain Res. Mol. Brain Res. 87:124-143(2001).  
 CC -1- FUNCTION: TERMINATES THE ACTION OF SEROTONINE BY ITS HIGH AFFINITY  
 CC SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS (By  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR  
 CC STIMULANTS SUCH AS AMPHETAMINES OR COCAINE (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER  
 CC FAMILY (SNF).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AF285761; AAF97247.1;  
 DR InterPro: IPR002437; 5HT\_transporter.  
 DR InterPro: IPR00175; Na/nttran\_symport.  
 DR Pfam: PF00209; SNF; 1.  
 DR Pfam: PF03491; 5HT\_transporter; 1.  
 DR Prodom: PD000448; Na/nttran\_symport.  
 DR PRINTS: PR00176; NANEUSMPORT.  
 DR PROSITE: PS00610; NA\_NEUROTAN\_SYM\_1; 1.  
 DR PROSITE: PS00754; NA\_NEUROTAN\_SYM\_2; 1.  
 DR PROSITE: PS0267; NA\_NEUROTAN\_SYM\_3; 1.  
 KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;  
 Symport.  
 FT DOMAIN 1 87 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 88 108 1 (POTENTIAL).  
 FT TRANSMEM 116 135 2 (POTENTIAL).  
 FT TRANSMEM 160 180 3 (POTENTIAL).  
 FT DOMAIN 181 252 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 253 271 4 (POTENTIAL).  
 FT TRANSMEM 280 297 5 (POTENTIAL).  
 FT TRANSMEM 333 350 6 (POTENTIAL).  
 FT TRANSMEM 362 383 7 (POTENTIAL).  
 FT TRANSMEM 417 436 8 (POTENTIAL).  
 FT TRANSMEM 464 482 9 (POTENTIAL).  
 FT TRANSMEM 498 518 10 (POTENTIAL).  
 FT TRANSMEM 539 558 11 (POTENTIAL).  
 FT TRANSMEM 577 595 12 (POTENTIAL).  
 FT DOMAIN 596 630 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 217 217 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SEQUENCE 630 AA; 70257 MW; 79DFBE59EB6924 CMC64;

Query Match Best Local Similarity 54.7%; Score 1717; DB 1; Length 630;  
 Matches 318; Conservative 97; Mismatches 156; Indels 16; Gaps 6;

OY 6 APPAPTAPP---DLPTAAKSRVSVSLTPARQRETKAKAEFLAVVGFADLGNW 62  
 DB 49 AVPSPGADDTGRHSIPAT-----TTLVAELHOGRETKGKVDLSTIGVAVDGLGNW 103

```

OY 63 RPPYICYONGGAGFLIPYCVMLLEFGLDPLFLELALGOYHRCGCTLTKRICPALKGVOY 122
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 104 RPPYICYONGGAGFLIPYCVMLLEFGLDPLFLELALGOYHRCGCTLTKRICPALKGVOY 163
OY 123 AICMIDIYMGWYNTITGMVYIYLASIASINSVLPMTSCDNEWTPLCTPYTSQOT--- 179
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 164 AICIAFAFYASYNTIMAMALYYLI---SFTDQPLMTSCKSNMTGCTNFESDNTJTW 220
OY 180 NPNSTPAKFEFFERVLFOHKSNGLDGPIKPSALFVFGVLYVYSIMKGVASACKV 239
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 221 TLHSTSPAEERTYRVLQIHNSKLDGJGSMQALCLMLFTYIYFSIMKGVATSGKV 280
OY 240 VVWVALADYVVLILLARGVTLPGATEGIRYLYPEPMHKLONSKYWIDAASQIFPSLPGC 299
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 261 VVWVATPFYIILSVLLVGGATLPGAMRGVLFYFLKNMCKLLETGVMIDAAGIIFPSLPGC 340
OY 300 FGTLLALSYNKNFNKNCRDALITSINCLNIFLAGFYIFSVLYGMVHVNKNSIEVGLE 359
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 341 FGVLLAFASYNKNFNKNCRDALITSINCLNIFLAGFYIFSVLYGMVHVNKNSIEVGLE 400
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 360 -GPGILFVYVPEALITMTGVSVMATITFFMLITLGLDSTFGGLVAVTALDCEYRVLGR 418
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 401 AGPSLFTFYAALANMPASTFFALITFLMLITLGLDSTFAGLEGVITRAVLDEFPHIMAK 460
OY 419 HREVFVAVLLFTYICALPTTYGGVYLVDLNLYGPGIALIFVFAEAGVCMVYGVDR 478
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 461 RREMFVAVLVITCFGLSVTLTFGAGVYVVKLEEVATGPAVLTALEAVNANSMWYGTQ 520
OY 479 FSEYRTMLGHTPGFMTCSYISPVFLVLFVSVLAHEMLGGEITYPSWSTTVGVN 538
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 521 FCRDVKEMLGSPGFMWRICVVAISPFLFLFICISPLRFLFOYNYPHMSITLGYC 580
OY 539 MTGTWSCIPLYIYIKLLITPCNCLNR--IKTQREPVTSIPADSTL 584
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 581 IGTSSFVCIPTIYIARLITRGTETREKRIKSTITPPEITPCGVARL 627

RESULT 5
S644_MOUSE
ID S644_MOUSE STANDARD: PRT: 630 AA.
AC 060857; 035241;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sodium-dependent serotonin transporter (5HT transporter) (5HTT).
GN SLC6A4 OR HTT OR SERT.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
    NCBI_TaxID=10090;
    [1]
RN RP SEQUENCE FROM N.A.
    RA MEDLINE=97189261; PubMed=9037532;
    RA Chang A.S., Chang S.M., Starnes D.M., Schroeter S., Bauman A.L.,
    RA Blakely R.D.;
    RA "Cloning and expression of the mouse serotonin transporter.";
    RL Brain Res. Mol. Brain Res. 43:185-192(1996).
    [2]
RN RP SEQUENCE FROM N.A.
    RA STRAIN=129;
    RC MEDLINE=97225900; PubMed=9073170;
    RA Bengel D., Hells A., Petri S., Seemann M., Glatz K., Andrews A.,
    RA Murphy D.L., Lesch K.P.;
    RA "Gene structure and 5'-flanking regulatory region of the murine
    RA serotonin transporter.";
    RL Brain Res. Mol. Brain Res. 44:286-292(1997).
    [3]
RN RP SEQUENCE OF 1-114 FROM N.A.
    RC STRAIN-BALB/c;
    RA Saito N., Sakai N., Kobayashi S., Fujimoto M., Morikawa O.,
    RA Ikegaki N.;
    RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
    [4]

```

```

RP SEQUENCE OF 69-630 FROM N.A.
RX MEDLINE=93283858; PubMed=8507984;
RA Gregor P., Patel A., Shlmade S., Lin C.L., Rochelle J.M., Kitayama S.,
RA Seldin M.F., Uhl G.R.;
RT "Murine serotonin transporter: sequence and localization to
    RT chromosome 11."
RL Mamm. Genome 4:283-284(1993).
CC -1- FUNCTION: TERMINATES THE ACTION OF SEROTONINE BY ITS HIGH
    CC AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
    CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
    CC -1- SIMILANTS SUCH AS AMPHETAMINES OR COCAINE.
    CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
    CC FAMILY (SNE).
    CC -1- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
    CC FRAMESHIFT IN POSITION 195.
    CC -----
    CC This SWISS-PROT entry is copyright. It is produced through a collaboration
    CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
    CC the European Bioinformatics Institute. There are no restrictions on its
    CC use by non-profit institutions as long as its content is in no way
    CC modified and this statement is not removed. Usage by and for commercial
    CC entities requires a license agreement (See http://www.isb-sib.ch/
    CC or send an email to license@isb-sib.ch).
    CC -----
DB EMBL: AF013604; AAB67172.1; -.
DB EMBL: Y08870; CAA70092.1; JOINED.
DB EMBL: Y08871; CAA70092.1; JOINED.
DB EMBL: Y08872; CAA70092.1; JOINED.
DB EMBL: Y08873; CAA70092.1; JOINED.
DB EMBL: Y08874; CAA70092.1; JOINED.
DB EMBL: Y08875; CAA70092.1; JOINED.
DB EMBL: Y08876; CAA70092.1; JOINED.
DB EMBL: Y08877; CAA70092.1; JOINED.
DB EMBL: Y08878; CAA70092.1; JOINED.
DB EMBL: Y08879; CAA70092.1; JOINED.
DB EMBL: Y08880; CAA70092.1; JOINED.
DB EMBL: U26452; AAB44750.1; -.
DB EMBL: X66119; -. NOT ANNOTATED. CDS.
DB MGD: MGI:96285; Slc6a4.
DB InterPro: IPR002437; 5HT_transporter.
DB InterPro: IPR000175; Na/nttran_symport.
DB Pfam: PF00209; SNE: 1.
DB Pfam: PF03491; 5HT_transporter; 1.
DB PRINTS: PR00176; NANUSMPORT.
DB PRODOM: PD000448; Na/nttran_symport; 1.
DB PROSITE: PS00610; NA_NEUROTRAN_SYM_1; 1.
DB PROSITE: PS00754; NA_NEUROTRAN_SYM_2; 1.
DB PROSITE: PS0267; NA_NEUROTRAN_SYM_3; 1.
KW Neurotransmitter transporter; transporter; Transmembrane; Glycoprotein;
    KW Symport.
FT DOMAIN 1 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 108 1 (POTENTIAL).
FT TRANSMEM 116 135 2 (POTENTIAL).
FT TRANSMEM 160 180 3 (POTENTIAL).
FT DOMAIN 181 252 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 253 271 4 (POTENTIAL).
FT TRANSMEM 280 297 5 (POTENTIAL).
FT TRANSMEM 333 350 6 (POTENTIAL).
FT TRANSMEM 362 383 7 (POTENTIAL).
FT TRANSMEM 417 436 8 (POTENTIAL).
FT TRANSMEM 464 482 9 (POTENTIAL).
FT TRANSMEM 498 518 10 (POTENTIAL).
FT TRANSMEM 539 558 11 (POTENTIAL).
FT TRANSMEM 577 595 12 (POTENTIAL).
FT DOMAIN 596 630 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 217 217 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 196 196 P -> Q (IN REF. 2).
FT CONFLICT 415 415 A -> R (IN REF. 2).
SQ SEQUENCE 630 AA; 70147 MW; F37EF1EC164FB30 CRC64;
Query Match 54.6%; Score 1716; DB 1; Length 630;

```







```

Db 401 AGPSLFTYAEAIANMPASTFEFAVFLMILITLGLDSTFAGLEGVITAVLDEPHVMAK 460
QY 419 HREVEVAUFLLEFYICALPTTYGGVYLDLNVYGPGLATLFVFAFAGVCMYGVDR 478
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 461 RREMFVLCVITTCFFGSLVTLFGCAVYKLEEFATPPALVTALIAVAVEMYGAINQ 520
QY 479 FSEEDRTMLGHTPGFMFRTCMYSISPVLVLFVFSVLAHEMLGCEYTPSMTITGVV 538
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 521 FCSOVKEMLGFSFGFMKICVNAISPFLFLFICFSFLMSPQRLRFQYDPRMSITLGYC 580
QY 539 MTGTTVSCIPLYIYIKLITPNCINR-IKTIQREPVSTPPADSTL 584
    : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 581 IGTSFICIPYIYIYRLVPTGLKERIKIGTPEPTPAIRPGDIRL 627

RESULT 8
S6A2_MOUSE STANDARD: PRT: 617 AA.
ID 56A2_MOUSE 05192:
AC 15-DEC-1998 (Rel. 37, Created)
DE 15-DEC-1998 (Rel. 37, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium-dependent noradrenaline transporter (norepinephrine
DE transporter) (NET).
GN SLC6A2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RA MEDLINE=98264327; PubMed=9603188;
RA Fritz J.D., Jayanthi L.D., Thoreson M.A., Blakely R.D.:
RT "Cloning and chromosomal mapping of the murine norepinephrine
RT transporter." 70:2241-2251(1998).
RL J. Neurochem. 70:2241-2251(1998).
CC -1- FUNCTION: TERMINATES THE ACTION OF NORADRENALINE BY ITS HIGH
CC AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
CC STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.
CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
CC FAMILY (SNF).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: U76306; AAB94302.1; -
CC MGD: MGI:1270850; SLC6A2.
CC InterPro: IPR001175; Na/ntan_symport.
DR DR P1am: PFO0209; SNF; 1.
DR DR PRINTS: PR00176; NANEUSMPORT.
DR DR PRODOM: PD000448; Na/ntan_symport; 1.
DR DR PROSITE: PS00610; NA_NEUROTRAN_SYM_2; 1.
DR DR PROSITE: PS00754; NA_NEUROTRAN_SYM_3; 1.
DR DR PROSITE: PS00757; NA_NEUROTRAN_SYM_3; 1.
KW Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
KW Symport.
FT DOMAIN 1 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 85 1 (POTENTIAL).
FT TRANSMEM 93 112 2 (POTENTIAL).
FT TRANSMEM 136 156 3 (POTENTIAL).
FT DOMAIN 157 234 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 235 253 4 (POTENTIAL).
FT TRANSMEM 262 279 5 (POTENTIAL).
FT TRANSMEM 315 332 6 (POTENTIAL).
FT TRANSMEM 344 365 7 (POTENTIAL).

```

```

FT TRANSMEM 398 417 8 (POTENTIAL).
FT TRANSMEM 444 462 9 (POTENTIAL).
FT TRANSMEM 478 498 10 (POTENTIAL).
FT TRANSMEM 519 538 11 (POTENTIAL).
FT TRANSMEM 557 575 12 (POTENTIAL).
FT CARBOHD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 617 AA; 69162 MW; AAB4412468BF59D CRC64;

Query Match
Best Local Similarity 51.9%; Score 1629.5; DB 1; Length 617;
Matches 310; Conservative 104; Mismatches 154; Indels 27; Gaps 9;

1 MPPSDAPPAPAPAP-----PDLPATTAQ-----KSRSVVSL-----TPARQETMAKKEF 47
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
6 MNPQVQPELGADPLPEQPLRCKRADLLVYKERNGVOCCLASQSDQAPRHWKCKIDF 65
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
48 LLAVGFVAVDLGNVWRFYICVONGGAFLLPYCYMLLEGGILPELLELAGQVHRCGL 107
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
66 LLSVGFVAVDLGNVWRFYICVONGGAFLLPYCYMLLEGGILPELLELAGQVHRCGL 125
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
108 TLKRICGALGVGAICMIDLYMGMYNTIIGAAVYLLIASINSVLPMTSCDNEMN 167
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
126 TWK-ICPFKGVGVAVILIALYGVFYNNVIAVSLVYLFSE-TLN--LPWTNCGHSMN 181
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
168 TPLCT-----PVTSPT--NPNSSTPAKEFEFFENNVLEQHSNGLDMDGPIKPSALCV 218
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
182 SPNCIDPKLLNLSVGLDHTKYSKYFETPAABEYENGVLHHESSGIDHIGLPQWLLCL 241
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
219 FGVEVLYVFSLSKGVRSAGKVVWATLAPVYVLLILARGVTLPGATGIRIYLTPEWHK 278
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
242 MVVIVLYVFSLSKGVRSAGKVVWATLAPVYVLLILARGVTLPGATGIRIYLTPEWHK 301
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
279 LONSVMVIDAASQIFSGPFGGLTLLASVKNFNKNYRDLNLSINCLTSPFAGVY 338
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
302 LKEATVWIDATQIFSGAGGVGLTAFASINKFENNCYRDLNLSINCLTSPFAGVY 361
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
339 FSVLYGMAYVONKSIEEVLGEGPGLVFIYVPEAATMTGSVFMAITFLMLITGLDSTF 398
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
362 FSLIYGMAYVONKSIEEVLGEGPGLVFIYVPEAATMTGSVFMAITFLMLITGLDSTF 421
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
399 GGLEAVTALCDEYRVRIGRIREVAVVALLFIYICALPTTYGGVYLDLNVYGPGLA 458
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
422 GGMFAVITGLADDF-QVLRHRKRLFTCVVITSTFLAFCITKGGIYVTLTDLTFAAGTS 480
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
459 ILFVFAEAGVCMYGVDRSEEDRTMLGHTPGFMFRTCMYSISPVLVLFVFSVLAH 518
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
481 ILFVFAEAGVCMYGVDRSEEDRTMLGHTPGFMFRTCMYSISPVLVLFVFSVLAH 540
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
519 EEMLGEEYTPSMTITGVWMTGTTVSCIPLYIYIKLITPNCINRIKTQREPE 573
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
541 KPLTYDYVTPPMANWVGMSIALSMILVPAVYIKFLIRGSLMERAVAYGITPE 595
    ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

RESULT 9
S6A2_BOVIN STANDARD: PRT: 615 AA.
ID 56A2_BOVIN P51143:
AC 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2001 (Rel. 40, Last annotation update)
DE Sodium-dependent noradrenaline transporter (norepinephrine
DE transporter) (NET).
GN SLC6A2 OR NORADR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
CX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE=adrenal medulla;
RA MEDLINE=94200377; PubMed=8150077;

```





CC -1- DISEASE: DEFECTS IN SLC6A2 ARE A CAUSE OF ORTHOSTATIC INTOLERANCE  
 CC (OI), A SYNDROME CHARACTERIZED BY LIGHTHEADEDNESS, FATIGUE,  
 CC ALTERED MENTATION AND SYMPOSE. IT IS ASSOCIATED WITH POSTURAL  
 CC TACHYCARDIA. PLASMA NOREPINEPHRINE CONCENTRATION IS ABNORMALLY  
 CC HIGH.  
 CC -1- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR  
 CC STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.  
 CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER  
 CC FAMILY (SNF).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL; M65105; AAAS9943.1; -;  
 CC EMBL; X91117; CA662566.1; JOINED.  
 CC EMBL; X91120; CA662566.1; JOINED.  
 CC EMBL; X91121; CA662566.1; JOINED.  
 CC EMBL; X91122; CA662566.1; JOINED.  
 CC EMBL; X91123; CA662566.1; JOINED.  
 CC EMBL; X91124; CA662566.1; JOINED.  
 CC EMBL; X91125; CA662566.1; JOINED.  
 CC EMBL; X91126; CA662566.1; JOINED.  
 CC EMBL; X91127; CA662566.1; JOINED.  
 CC EMBL; X91128; CA662566.1; JOINED.  
 CC EMBL; X91119; CA662566.1; JOINED.  
 CC PIR; S14278; S14278.  
 CC Gene; HGNC:11048; SLC6A2.  
 CC MIM; 604715; -;  
 CC InterPro: IPR000175; Na/nttran\_symport.  
 CC Pfam; PF00209; SNF; 1.  
 CC PRINTS; PR00176; NANEUSMPORT.  
 CC PRODOM; PD000448; Na/nttran\_symport; 1.  
 CC PROSITE; PS00610; NA\_NEUTROTAN\_SYM\_1; 1.  
 CC PROSITE; PS00754; NA\_NEUTROTAN\_SYM\_2; 1.  
 CC PROSITE; PS02067; NA\_NEUTROTAN\_SYM\_3; 1.  
 CC Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;  
 CC Symport; Disease mutation; Polymorphism;  
 CC DOMAIN 1 64  
 CC TRANSMEM 65 85  
 CC TRANSMEM 93 112  
 CC TRANSMEM 136 156  
 CC DOMAIN 157 234  
 CC TRANSMEM 235 253  
 CC TRANSMEM 262 279  
 CC TRANSMEM 315 332  
 CC TRANSMEM 344 365  
 CC TRANSMEM 398 417  
 CC TRANSMEM 444 462  
 CC TRANSMEM 478 498  
 CC TRANSMEM 519 538  
 CC TRANSMEM 557 575  
 CC DOMAIN 576 617  
 CC CARBOHYD 184 184  
 CC CARBOHYD 192 192  
 CC CARBOHYD 198 198  
 CC VARIANT 69 69  
 CC -----  
 CC VARIANT 99 99  
 CC VARIANT 245 245  
 CC VARIANT 292 292  
 CC VARIANT 356 356  
 CC VARIANT 369 369

FT VARIANT 375 375 N -> S (IN DBSNP:5567).  
 FT FT /FTid=VAR\_011762.  
 FT VARIANT 457 457 A -> P (IN OI: LOSS OF FUNCTION).  
 FT FT /FTid=VAR\_010022  
 FT VARIANT 463 463 K -> R (IN DBSNP:5570).  
 FT FT /FTid=VAR\_011763.  
 FT VARIANT 478 478 G -> S (IN DBSNP:1805067).  
 FT FT /FTid=VAR\_011764.  
 FT VARIANT 528 528 F -> C (IN DBSNP:5558).  
 FT FT /FTid=VAR\_011765  
 FT VARIANT 548 548 Y -> H (IN DBSNP:5559).  
 FT FT /FTid=VAR\_011766.  
 FT SEQUENCE 617 AA: 69332 MW: BDC6DF31316907BB CRC64;  
 SO  
 Query Match 51.1%; Score 1605.5; DB 1; Length 617;  
 Best local similarity 51.6%; Pred. No. 4.6e-98;  
 Matches 307; Conservative 106; Mismatches 155; Indels 27; Gaps 10;  
 QY 1 MPPSDAPP--APPAAPPDLPA-TTAQ---KSRSVVSLT---PARORETAKKAEE 47  
 DB 6 MNPQVPEPNNAGADTGEQPLBARRTAELLVYKERNVGCLLAPRDGAQPRETWGKKIDF 65  
 QY 48 LLAYGFAVDLGNVRFYICQNGGAFLLPYCMLLFGGLPLFLELALGQYHRCCL 107  
 DB 66 LLSVGFVAVDLANWRFPLCYCKNGGAFLLPYLFLFLIACMPLEFYMELALGOYNREGAA 125  
 QY 108 TLMKRIPCALKGVGAICMIDYMGMYNTIIGNAVYLLIASLSINSVLPWTSQDNEMN 167  
 DB 126 TWMK-ICPFPGKGVAVLLIALYGFYVNIANSLLYLFSSP-TLN--LWMTDGGHWN 181  
 QY 168 TPLCT-----PVTSPT--NPNSSTPAKEEFFERNVLEQHSNGLDMDGPIKPSLALCV 218  
 DB 182 SPNCTDPKLLNGSVLGNHTKYSKYKFTPAEYERGVHLHSSGIDHIGLPQMOLLCL 241  
 QY 219 FGVFLVYFSLMKGYRSAGKVVWYATAPYVLLILLARGTLPGATGIRVYLPREHK 278  
 DB 242 MYYVIVLVFSLSMKGKVTSGKVVWYATAPYVLLVHGVTLVLPASNGINAVLHIDYR 301  
 QY 279 LQNSKVMIDAAQSQTFSPGFGTLLALSYNKFNENNCYRALTLTSSINCLTSPFLAGFVI 338  
 DB 302 LKERTVWIDANTQIFFSIAGAGFVLIAPASNKKPNCKNRALLTSSINCLTSPFGFVI 361  
 QY 339 FSVLGYMAHVONKSTIEVGLGPGPLVTPYEDATATMGVPMALIFPLMLITGLDSTF 398  
 DB 362 FSLISGYMAHEKVNIEDVATGAGLVFLYPEALISTLSGSTFMVAVFEVMLALGLDSSM 421  
 QY 399 GGLVETATLDDVPRVGRHREVEVAVLLFIYCALPTTYGGVAVDILLVYGPGLA 458  
 DB 422 GGMVAVITGLADDF-QVLRHRRKLETFGVSTFLLALFCLTKGGIVYLLLDPPFAAGTS 480  
 QY 459 ILFVFAEAGVGVYGVDRSEEDVRTMLGHTPGMFMRTGMSYISPYELLVLFVSVLAH 518  
 DB 481 ILFVFLMAGISVMSYGVDRSNDIQMGMRPGIYMWLCMKRFPALLLVYVVSIIIN 540  
 QY 519 EEMIGGEYTVYSWSTVGVWMTGTTVSCIPLYIKLLITPGCNINRIKTTORPE 573  
 DB 541 KPLTVDYIIFPMANWVGMSIALSSMLVPIYVYIKFLSTGSIEMERLAVGITPE 595  
 RESULT 11  
 S6A3\_BOVIN  
 ID S6A3\_BOVIN STANDARD: PRT: 693 AA.  
 AC P27922;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Sodium-dependent dopamine transporter (DA transporter) (DAT).  
 GN SLC6A3.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;





QY 429 LFIYICALPTTGGVYLVDLLNVYGPGLAILEFVFAEAGVGVYGVDRSEDEVRTMG 488  
 DB 454 LATFLLSLFCVTNGIYFTLLDHFRAAGSILFGLVLEAGVAMFYGVGGFSDDIQOMTG 513  
 QY 489 HTPGFWRTGWSYISPVLLVLFVSVLAHEMLGGEYTYSSWTGVMGTGTVSCIP 548  
 DB 514 QRPSTLYMRLCKWLKSPCLLFVYVVSIVTFRRPHYGAVIFPDMANALGVITSSMAVP 573  
 QY 549 LYIYKLLITPGNCINRIKTIQRE 573  
 DB 574 IYAYKFCSLPESFEKRLAYIAPE 598

RESULT 13  
 SGA3\_RAT STANDARD: PRT: 619 AA.  
 AC P23977.  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 GN Sodium-dependent dopamine transporter (DA transporter) (DAT).  
 OS Rattus norvegicus (rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92054540; PubMed=1948035;  
 RA Kilty J.E., Loring D., Amara S.G.;  
 RT "Cloning and expression of a cocaine-sensitive rat dopamine  
 transporter.";  
 RL Science 254:578-579(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92054539; PubMed=1948034;  
 RA Shimada S., Kitayama S., Lin C.-L., Patel A., Nanthakumar E.,  
 RA Gregor P., Kuhar M., Uhl G.;  
 RT "Cloning and expression of a cocaine-sensitive dopamine transporter  
 complementary DNA.";  
 RL Science 254:576-578(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92111727; PubMed=1765147;  
 RA Giros B., el Mestikawy S., Bertrand L., Caron M.G.;  
 RT "Cloning and functional characterization of a cocaine-sensitive  
 dopamine transporter.";  
 RL FEBS Lett. 295:149-154(1991).  
 RN [4]  
 RP MUTAGENESIS.  
 RX MEDLINE=92365546; PubMed=1502198;  
 RA Kitayama S., Shimada S., Xu H., Markham L., Donovan D.M., Uhl G.;  
 RT "Dopamine transporter site-directed mutations differentially alter  
 substrate transport and cocaine binding.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:7782-7785(1992).  
 CC -1- FUNCTION: TERMINATES THE ACTION OF DOPAMINE BY ITS HIGH  
 AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR  
 STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.  
 CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER  
 FAMILY (SMF).  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation  
 at the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL, M80570; AAA73143.1; -  
 CC DR

DR EMBL, M80570; AAA73143.1; -  
 DR EMBL, S76145; AAB21099.1; -  
 DR PIR, S20346; S20346.  
 DR InterPro: IPR000175; Na/ntran\_symport.  
 DR Pfam: PF00209; SNF; 1.  
 DR PRINTS: PR00176; NANEUSMPORT.  
 DR PRODOM: PD000448; Na/ntran\_symport; 1.  
 DR PROSITE: PS00610; NA\_NEUOTRAN\_SYM\_1; 1.  
 DR PROSITE: PS00754; NA\_NEUOTRAN\_SYM\_2; 1.  
 DR PROSITE: PS00267; NA\_NEUOTRAN\_SYM\_3; 1.  
 KW Neurotransmitter transporter; Transport; Transmembrane; Glycoprotein;  
 KW Symport.  
 FT DOMAIN 1 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 1 (POTENTIAL).  
 FT TRANSMEM 96 116 2 (POTENTIAL).  
 FT TRANSMEM 140 160 3 (POTENTIAL).  
 FT DOMAIN 161 236 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 237 255 4 (POTENTIAL).  
 FT TRANSMEM 264 281 5 (POTENTIAL).  
 FT TRANSMEM 317 334 6 (POTENTIAL).  
 FT TRANSMEM 346 367 7 (POTENTIAL).  
 FT TRANSMEM 400 419 8 (POTENTIAL).  
 FT TRANSMEM 446 464 9 (POTENTIAL).  
 FT TRANSMEM 480 500 10 (POTENTIAL).  
 FT TRANSMEM 521 540 11 (POTENTIAL).  
 FT TRANSMEM 559 577 12 (POTENTIAL).  
 FT DOMAIN 578 619 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 597 597 E -> K (IN REF. 3).  
 SQ SEQUENCE 619 AA; 68746 MW; DF3A30C981095D24 CRC64;

Query Match 49.0%; Score 1339; DB 1; Length 619;  
 Best Local Similarity 49.4%; Pred. No. 1e-93;  
 Matches 280; Conservative 105; Mismatches 156; Indels 26; Gaps 5;

QY 14 PDDLPTATTAQKRSRVVSLTPARORETNAKKRFEFLAVGVAVDIGNVWRPFYICYONGG 73  
 DB 50 PPTP-----VEAQRERTWSKIDFLSVGVAVDIGNVWRPFYICYONGG 95  
 QY 74 GAFLLPYCVMLFGLPLFLELALGOVHRCCLTLMKRICPALKGVAICIMDIYMG 133  
 DB 96 GAFLLPYVLLFWYIACMLPLFYMELALGOFRBEAAGVWK-ICVNLGVGFTVLLISFYGE 154  
 QY 134 YNVTIIGAAVYLLIASLINSVLPWTSQDNEMWPLCTPVTSPTNPN-----SSTP 186  
 DB 155 FYNVIIAMALHYF---FSSFTMDLPIMHCNNTWNSPNCSDAHASNSDGLINDTFGTPP 211  
 QY 187 AKFEFRNVLEQHKNSGDDMGRIKPSLALCVGVFVLVYFSLMKGVRSAGVWVWTLA 246  
 DB 212 AAEYFERGVHLHOSRGIDDLGPPKQMLTACLVLYLVLYFLMKGVKSGVWVWITNM 271  
 QY 247 PYYVLLILLARVTLPGATEGIRYVLTPEMKLQNSKWIIDAASOIFSLGFGFTLLAL 306  
 DB 272 PYYVLLILLARVTLPGATEGIRYVLTPEMKLQNSKWIIDAASOIFSLGFGFTLLAL 331  
 QY 307 SSYNFNNKCYDALITSSINCLTSFLAGFVYFSLGVAAHQNSIEVGLGGLVFI 366  
 DB 332 SSYNFNNKCYDALITSSINCLTSFLAGFVYFSLGVAAHQNSIEVGLGGLVFI 391  
 QY 367 VYPEAIATPTGVSFVNAIIFELMLITLGLDSTFGGLGAVTTALCDEPVRVLRHREVFVAV 426  
 DB 392 IYPEAIATPLSSANAAYVFFMLLTLGLDISAMGHSYTTGLVDFE-QLLHHRRELFTLG 450  
 QY 427 LLLFYICALPTTGGVYLVDLLNVYGPGLAILEFVFAEAGVGVYGVDRSEDEVRTMG 486  
 DB 451 IYLAIFLLSLFCVTNGIYFTLLDHFRAAGSILFGLVLEAGVAMFYGVGGFSDDIQOM 510  
 QY 487 ICHTGWFWRTGWSYISPVLLVLFVSVLAHEMLGGEYTYSSWTGVMGTGTVSCIP 546  
 DB 511 TGORPNLWRLCKWLKSPCLLFVYVVSIVTFRRPHYGAVIFPDMANALGVITSSMAVP 570

OY 547 IPLYIYKLLITPGNCINRIKTIORPE 573  
 DB 571 VPIATYKFCSLPGSFREKLAVATPE 597

RESULT 14  
 56A3\_MOUSE  
 ID 56A3\_MOUSE STANDARD: PRT: 619 AA.  
 AC 061327, 060719, 09R112;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Sodium-dependent dopamine transporter (DA transporter) (DAT).  
 GN SLC6A3 OR DAT1 OR DAT.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;

SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RX MEDLINE=99307154; PubMed=10373632;  
 RA Wu X., Gu H.H.;  
 RT "Molecular cloning of the mouse dopamine transporter and  
 RL pharmacological comparison with the human homologue.";  
 RL Gene 233:163-170(1999).  
 RN [2]  
 RP SEQUENCE OF 1-343 FROM N.A.  
 RC STRAIN=BAB/c; TISSUE=Brain;  
 RX MEDLINE=95364623; PubMed=7637582;  
 RA Donovan D.M., Vandenberg D.J., Perry M.P., Bird G.S., Ingersoll R.,  
 RA Nanthakumar E., Uhl G.R.;  
 RT "Human and mouse dopamine transporter genes: conservation of  
 5'-flanking sequence elements and gene structures.";  
 RL Brain Res. Mol. Brain Res. 30:327-335(1995).  
 CC -1- FUNCTION: TERMINATES THE ACTION OF DOPAMINE BY ITS HIGH  
 CC AFFINITY SODIUM-DEPENDENT REUPTAKE INTO PRESYNAPTIC TERMINALS.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).  
 CC -1- MISCELLANEOUS: THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR  
 CC STIMULANTS SUCH AS AMPHETAMINES OR COCAINE.  
 CC -1- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER  
 CC FAMILY (SNF).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AF109072; AAD19643.1;  
 CC EMBL: U15791; AA86462.1;  
 CC EMBL: U12313; AA86462.1; JOINED.  
 CC EMBL: U16265; AAC52283.1;  
 CC MGD: MGI:94862; SLC6A3.  
 CC InterPro: IPR001175; Na/ntran\_symport.  
 CC Pfam: PF00209; SNF.1.  
 CC PRINTS: PR00176; NANEUSMPORT.  
 CC PRODOM: PD000448; Na/ntran\_symport.1.  
 CC PROSITE: PS00610; NA\_NEUOTRAN\_SYM\_1; 1.  
 CC PROSITE: PS00754; NA\_NEUOTRAN\_SYM\_2; 1.  
 CC PROSITE: PS0267; NA\_NEUOTRAN\_SYM\_3; 1.  
 CC Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;  
 CC Symport.  
 CC KW DOMAIN 1 68 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 69 89 1 (POTENTIAL).  
 CC TRANSMEM 96 116 2 (POTENTIAL).  
 CC TRANSMEM 140 160 3 (POTENTIAL).  
 CC DOMAIN 161 236 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 237 255 4 (POTENTIAL).  
 CC TRANSMEM 264 281 5 (POTENTIAL).  
 CC [1]

FT TRANSMEM 317 334 6 (POTENTIAL).  
 FT TRANSMEM 346 367 7 (POTENTIAL).  
 FT TRANSMEM 400 419 8 (POTENTIAL).  
 FT TRANSMEM 446 464 9 (POTENTIAL).  
 FT TRANSMEM 480 500 10 (POTENTIAL).  
 FT TRANSMEM 521 540 11 (POTENTIAL).  
 FT TRANSMEM 559 577 12 (POTENTIAL).  
 FT DOMAIN 578 619 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 181 181 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT CARBOHYD 188 188 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT CARBOHYD 196 196 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT CARBOHYD 204 204 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 SQ SEQUENCE 619 AA: 68805 MW: 7436137BC6461E9B CRC64;

Query Match 49.0%; Score 1538; DB 1; Length 619;  
 Best Local Similarity 49.4%; Pred. No. 1,2e+93;  
 Matches 280; Conservative 104; Mismatches 157; Indels 26; Gaps 5;

OY 14 PDDLPTATTAOKRSRVASLTPARORETWAKAEFLAVGVAVDGNVRRPYICYONGG 73  
 DB 50 PQQT-----VEQEREWTKSKIDFLSYIGFVADLANVRRPYLCYKNG 95  
 OY 74 GAFLLPYCVMLLEGGPLFFLELALGOYHRCGLTLMKRICPALKGVAICMIDYWG 133  
 DB 96 GAFLLPYLLFMVYAGMPLFYWMELALGQFNREGAGVMK-ICPVLLKGVFYLLISFYGF 154  
 OY 134 YNTTIGAAVYLLASLANSVLPWTSCDMENMTPLCTPYTSPTNTN-----SSTP 186  
 DB 155 FYNVIIAALHYF--FSSFTMDLPWICHNNWNPNCSDAHSSSDGLGNDTFGTTP 211  
 OY 187 AKEFFERNVLEQHSNGSLDMQPIKPSLALCFGVFLVYSLMKGVASACKVWVWVATA 246  
 DB 212 AAEEFERGVLLHQSRIIDDLGPPRMQTLACLVLYVLLYSIMKGVATSKVWVWITATM 271  
 OY 247 PYVULLLLARCVLPAGTEGIRYLPPEMKLQNSKWDIAASQIFSLGPGCTLLAL 306  
 DB 272 PYVULLLLARCVLPAGMDGIRAYLSVDFRLCASVWIDAAQVCSLGVFVLTAF 331  
 OY 307 SSYNNFNCCRDALITSSINCLTFSLAGFYFVSFGMAVQNSIEVGLGGLVFI 366  
 DB 332 SSYNNFTNCRDAITITTSINSLTSFSSGFVYFSLGIMACKHNPIPIVADTDGGLFI 391  
 OY 367 VYPEAIATMGTSVFNAIFFMLITLGLDSTFGGLAVTTALCODEYPRVILGRHREYAV 426  
 DB 392 IYPEAIATPLISSAAVAFFMLITLGLDSAMGMSVITGLVDF-QLLRHRELFTLG 450  
 OY 427 LLLFYIALPPTTYGAYLVLDLNVGPGALILFVFAEAGVGVVGVDRFSQDVDTM 486  
 DB 451 IYLAFFLLSLFCVYNGGIYVFTLLDHFAGSILFGLVLEAIGVAMFYGVQOFSDDIKQM 510  
 OY 487 LGHTGWFMRQMSYISPVFLVLFVFSVLAEHEMLGEGYVPSISIVGWMMGTTCVSC 546  
 DB 511 TGQRNLYWRCKMKLVSPCLLYVYVSVIVFRPHYGAIFYPDMANLGMITSSNAM 570  
 OY 547 IPLYIYKLLITPGNCINRIKTIORPE 573  
 DB 571 VPIATYKFCSLPGSFREKLAVATPE 597

RESULT 15  
 NTDQ\_CAEEL STANDARD: PRT: 615 AA.  
 ID NTDQ\_CAEEL 09XTRK;  
 AC 01-FEB-1994 (Rel. 28, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Sodium-dependent dopamine transporter (DA transporter) (DAT).  
 GN T2365.5.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Felodertinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]





